This listing of claims will replace all prior versions, and listings, of claims in the application:

## Listing of Claims:

Claims 1-24 (canceled)

Claim 25 (new)    An isolated nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, and a complement thereof.

Claim 26 (new)    A nucleic acid fragment comprising at least a 20 contiguous base pair segment of the isolated nucleic acid sequence of claim 25.

Claim 27 (new)    The nucleic acid fragment of claim 26 comprising a 20-30 contiguous base pair segment of the isolated nucleic acid sequence of claim 25.

Claim 28 (new)    A primer comprising the nucleic acid fragment of claim 26.

Claim 29 (new)    A probe comprising the nucleic acid fragment of claim 26.

Claim 30 (new)    The isolated nucleic acid sequence of claim 25, wherein at least one preferred codon replaces at least one codon of said sequence.

Claim 31 (new)    An amino acid sequence coded by the isolated nucleic acid sequence of claim 25.

Claim 32 (new)    The amino acid sequence of claim 31, wherein said amino acid sequence is selected from SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID

NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID
NO:39, SEQ ID NO:41, and SEQ ID NO:42.


Claim 33 (new)     A peptide comprising at least a 10 contiguous amino acid segment
of the amino acid sequence of claim 32.


Claim 34 (new)     The peptide of claim 33 comprising a 10-20 contiguous amino acid
segment of the amino acid sequence of claim 32.


Claim 35 (new)     An expression vector comprising the isolated nucleic acid
sequence of claim 25, said sequence operably-linked to control elements for the
expression of said sequence in a host cell.


Claim 36 (new)     A host cell transfected with the expression vector of claim 35.


Claim 37 (new)     An antisense oligonucleotide comprising a 10-40 contiguous base
pair segment of a reverse complement of a nucleic acid sequence selected from SEQ
ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8,
SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID
NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, and SEQ ID NO:21.


Claim 38 (new)     A method for detecting the presence of at least one variant nucleic
acid sequence of obesity and/or diabetes related genes in a biological sample
comprising the steps of:

     (a)     hybridizing to nucleic acid material of the biological sample an isolated
            nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ
            ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
            SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID
            NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21,
            or a complement thereof; and

     (b)     detecting a hybridization complex produced by step (a);

wherein the presence of the hybridization complex correlates with the presence of at
least one variant nucleic acid sequence in the biological sample.

Claim 39 (new)    A method for determining the level of variant nucleic acid sequences in a biological sample comprising the steps of:

    (a)    hybridizing to nucleic acid material of the biological sample an isolated nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, or a complement thereof;

    (b)    determining the amount of hybridization complexes produced by step (a); and

    (c)    normalizing the amount of hybridization complexes to provide a level of variant nucleic acid sequences in the biological sample.

Claim 40 (new)    A method for determining the ratio between the level of a nucleic acid sequence of an obesity and/or diabetes related gene variant in a first biological sample and a variant produced by alternative splicing in a second biological sample comprising the steps of:

    (a)    determining the level of a first nucleic acid sequence of an obesity and/or diabetes related gene variant in a first biological sample;

    (b)    determining the level of a second nucleic acid sequence of an alternative splicing form of the variant in a second biological sample; and

    (c)    comparing the levels obtained in step (a) and step (b) to give a ratio.

Claim 41 (new)    The method of claim 40, wherein the first biological sample and the second biological sample are the same sample.

Claim 42 (new)    The method of claim 40, wherein the first nucleic acid sequence and the second nucleic acid sequence are mRNA transcripts.

Claim 43 (new)    The method of claim 42, wherein the first nucleic acid sequence and the second nucleic acid sequence are deposed on a nucleic acid chip.

Claim 44 (new)    A method for the identification of compounds capable of affecting the binding affinity of obesity and/or diabetes related proteins to the receptors of said proteins comprising the steps of:

    (a)     providing an amino acid sequence selected from SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:41, and SEQ ID NO:42;

    (b)     contacting a candidate compound with the amino acid sequence in the presence of at least one receptor of an obesity and/or diabetes related gene;

    (c)     determining the effect of the candidate compound on the binding of the amino acid sequence to the at least one receptor; and

    (d)     selecting a compound capable of affecting the binding affinity of obesity and/or diabetes related proteins to the receptors of said proteins.

Claim 45 (new)    A method for determining the ratio between the level of an obesity and/or diabetes related protein variant in a first biological sample and a variant produced by alternative splicing in a second biological sample comprising the steps of:

    (a)     determining the level of a first amino acid sequence of an obesity and/or diabetes related gene variant in a first biological sample;

    (b)     determining the level of a second amino acid sequence of an alternative splicing form of the variant in a second biological sample; and

    (c)     comparing the levels obtained in step (a) and step (b) to give a ratio.

Claim 46 (new)    A method of detecting a specific obesity and/or diabetes related nucleic acid sequence by polymerase chain reaction comprising the steps of:

    (a)     amplifying a specific obesity and/or diabetes related nucleic acid sequence with a primer pair, wherein at least one of the primers comprises an at least 20 contiguous base pair segment of a nucleic acid sequence selected from SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16,

SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:21, and a complement thereof; and

(b)     detecting the nucleic acid product of step (a).